## SEQUENCE LISTING

```
<110> Ajinomoto Co., Inc.
<120> A method of secreting and producing proteins
<130> Y1J0182
<140>
<141>
<150> JP 2001-98808
<151> 2001-03-30
<160> 60
<170> PatentIn Ver. 2.1
<210> 1
<211> 43
<212> PRT
<213> Corynebacterium glutamicum
<400> 1
Met Arg Asp Thr Ala Phe Arg Ser Ile Lys Ala Lys Ala Gln Ala Lys
                                      10
Arg Arg Ser Leu Trp Ile Ala Ala Gly Ala Val Pro Thr Ala Ile Ala
Leu Thr Met Ser Leu Ala Pro Met Ala Ser Ala
                              40
<210> 2
 <211> 30
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 2
 Met Phe Asn Asn Arg Ile Arg Thr Ala Ala Leu Ala Gly Ala Ile Ala
 Ile Ser Thr Ala Ala Ser Gly Val Ala Ile Pro Ala Phe Ala
                                   25
 <210> 3
 <211> 25
 <212> PRT
 <213> Corynebacterium ammoniagenes
 Met Lys Arg Met Lys Ser Leu Ala Ala Ala Leu Thr Val Ala Gly Ala
 Met Leu Ala Ala Pro Val Ala Thr Ala
```

٠,

```
<210> 4
<211> 782
<212> DNA
<213> Corynebacterium glutamicum
<220>
<221> CDS
<222> (579)..(782)
<400> 4
aaattootgt gaattagotg atttagtact tttoggaggt gtotattott accaaatogt 60
caagttgtgg gtagagtcac ctgaatatta attgcaccgc acgggtgata tatgcttatt 120
tgctcaagta gttcgaggtt aagtgtattt taggtgaaca aatttcagct tcgggtagaa 180
gactttcgat gcgcttcaga gcttctattg ggaaatctga caccacttga ttaaatagcc 240
taccccgaa ttgggggatt ggtcattttt tgctgtgaag gtagttttga tgcatatgac 300
ctgcgtttat aaagaaatgt aaacgtgatc agatcgatat aaaagaaaca gtttgtactc 360
aggtttgaag cattttctcc gattcgcctg gcaaaaatct caattgtcgc ttacagtttt 420
tetcaacgae aggetgetaa getgetagtt eggtggeeta gtgagtggeg tttaettgga 480
taaaagtaat cccatgtcgt gatcagccat tttgggttgt ttccatagca atccaaaggt 540
ttcgtctttc gatacctatt caaggagcct tcgcctct atg ttt aac aac cgt atc 596
                                           Met Phe Asn Asn Arg Ile
                                                              5
                                             1
cgc act gca gct ctc gct ggt gca atc gca atc tcc acc gca gct tcc
                                                                    644
Arg Thr Ála Ála Leu Ála Gly Ála Ile Ála Ile Ser Thr Ála Ála Ser
                                  15
              10
 ggc gta gct atc cca gca ttc gct cag gag acc aac cca acc ttc aac
                                                                    692
 Gly Val Ala Ile Pro Ala Phe Ala Gln Glu Thr Asn Pro Thr Phe Asn
                              30
          25
 atc aac aac ggc ttc aac gat gct gat gga tcc acc atc cag cca gtt
                                                                    740
 Ile Asn Asn Gly Phe Asn Asp Ala Asp Gly Ser Thr Ile Gln Pro Val
      40
                                                                    782
 gag cca gtt aac cac acc gag gaa acc ctc cgc gac ctg act
 Glu Pro Val Asn His Thr Glu Glu Thr Leu Arg Asp Leu Thr
                                           65
                      60
  55
 <210> 5
 <211> 68
 <212> PRT
 <213> Corynebacterium glutamicum
```

<400> 5 Met Phe Asn Asn Arg Ile Arg Thr Ala Ala Leu Ala Gly Ala Ile Ala Ile Ser Thr Ala Ala Ser Gly Val Ala Ile Pro Ala Phe Ala Gln Glu Thr Asn Pro Thr Phe Asn Ile Asn Asn Gly Phe Asn Asp Ala Asp Gly 35 Ser Thr Ile Gln Pro Val Glu Pro Val Asn His Thr Glu Glu Thr Leu Arg Asp Leu Thr 65 <210> 6 <211> 1809 <212> DNA <213> Streptoverticillium mobaraense <220> <221> CDS <222> (578)..(1798) <400> 6 gtcgacgcgg gccgggaggg ggtgcggcgg cgcccttcgg ctgtgtggac gaagcgtcgg 60 gtcggagggg cggccggata tcgtccttgg ggcggggtgg ccggaattgc cgccatggtg 120 ttgccgggga atcgacccga agacatgatc acttctcgta tccacccgat cacgtatccg 180 ggagtcgaga agtgttacgc cgtgcccctg tccgcgtcct cacccctgtc gccgtgacag 240 cgacccgcgt tcttccactc gcacggacgg ccccacagga cctttcggcc cgggctcgcc 300 ccgccgcctc ggtgacggcc tccgaataac gcggccgccg gggcctcggc cggttgaccg 360 atcegggtca egegeeeege egggegggeg gecaegteeg gtetegeeee geeegaeate 420 ggctgcgact gccttcgctc gcacttcttc ccgcctcccg gccgcgtttt tccgccgccg 480 aaggtgegge gaegegtaee gaateeeet teategegae gtgetteege aeggeegegt 540 tcaacgatgt tccacgacaa aggagttgca ggtttcc atg cgc ata cgc cgg aga 595 Met Arg Ile Arg Arg Arg 643 gct ctc gtc ttc gcc act atg agt gcg gtg tta tgc acc gcc gga ttc Ala Leu Val Phe Ala Thr Met Ser Ala Val Leu Cys Thr Ala Gly Phe 10 atg ccg tcg gcc ggc gag gcc gcc gcc gac aat ggc gcg ggg gaa gag 691 Met Pro Ser Ala Gly Glu Ala Ala Ala Asp Asn Gly Ala Gly Glu Glu

٠,

30

acg Thr	aag Lys 40	tcc Ser	tac Tyr	gcc Ala	gaa Glu	acc Thr 45	tac Tyr	cgc Arg	ctc Leu	acg Thr	gcg Ala 50	gat Asp	gac Asp	gtc Val	gcg Ala	739
aac Asn 55	atc Ile	aac Asn	gcg Ala	ctc Leu	aac Asn 60	gaa Glu	agc Ser	gct Ala	ccg Pro	gcc Ala 65	gct Ala	tcg Ser	agc Ser	gcc Ala	ggc Gly 70	787
ccg Pro	tcg Ser	ttc Phe	cgg Arg	gcc Ala 75	ccc Pro	gac Asp	tcc Ser	gac Asp	gac Asp 80	agg Arg	gtc Val	acc Thr	cct Pro	ccc Pro 85	gcc Ala	835
gag Glu	ccg Pro	ctc Leu	gac Asp 90	agg Arg	atg Met	ccc Pro	gac Asp	ccg Pro 95	tac Tyr	cgt Arg	ccc Pro	tcg Ser	tac Tyr 100	ggc Gly	agg Arg	883
gcc Ala	gag Glu	acg Thr 105	gtc Val	gtc Val	aac Asn	aac Asn	tac Tyr 110	ata Ile	cgc Arg	aag Lys	tgg Trp	cag Gln 115	cag Gln	gtc Val	tac Tyr	931
agc Ser	cac His 120	cgc Arg	gac Asp	ggc Gly	agg Arg	aag Lys 125	cag Gln	cag Gln	atg Met	acc Thr	gag Glu 130	gag Glu	cag Gln	cgg Arg	gag Glu	979
tgg Trp 135	Leu	tcc Ser	tac Tyr	ggc Gly	tgc Cys 140	gtc Val	ggt Gly	gtc Val	acc Thr	tgg Trp 145	val	aat Asn	tcg Ser	ggt	cag Gln 150	1027
tac Tyr	ccg Pro	acg Thr	aac Asn	aga Arg 155	Leu	gcc Ala	ttc Phe	gcg Ala	tcc Ser 160	Phe	gac Asp	gag Glu	gac Asp	agg Arg 165	Pne	1075
aag Lys	aac Asn	gag Glu	ctg Leu 170	ı Lys	aac Asn	ggc Gly	agg Arg	ccc Pro 175	Arg	tcc Ser	ggc Gly	gag Glu	acq Thi 180	Arg	gcg Ala	1123
gaç Glu	g tto 1 Phe	gaç Glu 185	ı Gly	c cgc / Arc	gto g Val	gcg Ala	aag Lys 190	Glu	g ago i Ser	tto Phe	c gad e Asp	gaç Glu 195	1 GI	g aaq ı Lys	g Gly	: 1171
tto Phe	c caq e Glr 200	n Arq	g gco g Ala	g cgt a Aro	gaq g Glu	g gtg ı Val 205	. Ala	g tco a Ser	gto Val	ato L Met	g aad t Asi 210	n Are	g gc	c cto	g gaq ı Glu	g 1219 1
aac Asi 21	n Ala	c cad a His	c gad s Asj	c gad o Gli	g ago u Se: 22	c gct r Ala O	tac a Tyr	c cto	c gad ı Ası	e aad Asi 22	n Le	c aa u Ly	g aa s Ly	g ga s Gl	a cto u Leo 23	1
gc Al	g aa a As	c gg n Gl	c aa y As	c ga n As; 23	p Al	c cto a Le	g cgo u Aro	c aa g Ası	c gad n Gl	u As	c gc p Al	c cg a Ar	t tc g Se	c cc r Pr 24	O PII	c 1315 e
ta Ty	c tc r Se	g gc r Al	g ct a Le 25	u Ar	g aa g As	c ac n Th	g cc r Pr	g tc o Se 25	r Ph	c aa e Ly	g ga s Gl	g cg u Ar	g aa g As 26	n GI	a gg y Gl	с 1363 У

. .

aat Asn	cac His	gac Asp 265	ccg Pro	tcc Ser	agg Arg	atg Met	aag Lys 270	gcc Ala	gtc Val	atc Ile	tac Tyr	tcg Ser 275	aag Lys	cac His	ttc Phe	1411
tgg Trp	agc Ser 280	ggc Gly	cag Gln	gac Asp	cgg Arg	tcg Ser 285	agt Ser	tcg Ser	gcc Ala	gac Asp	aag Lys 290	agg Arg	aag Lys	tac Tyr	ggc Gly	1459
gac Asp 295	ccg Pro	gac Asp	gcc Ala	ttc Phe	cgc Arg 300	ccc Pro	gcc Ala	ccg Pro	ggc Gly	acc Thr 305	ggc Gly	ctg Leu	gtc Val	gac Asp	atg Met 310	1507
tcg Ser	agg Arg	gac Asp	agg Arg	aac Asn 315	att Ile	ccg Pro	cgc Arg	agc Ser	ccc Pro 320	acc Thr	agc Ser	ccc Pro	ggt Gly	gag Glu 325	gga Gly	1555
ttc Phe	gtc Val	aat Asn	ttc Phe 330	Asp	tac Tyr	ggc Gly	tgg Trp	ttc Phe 335	ggc Gly	gcc Ala	cag Gln	acg Thr	gaa Glu 340	gcg Ala	gac Asp	1603
gcc Ala	gac Asp	aag Lys 345	Thr	gtc Val	tgg Trp	acc Thr	cac His 350	GTĀ	aat Asn	cac His	tat Tyr	cac His 355	пта	ccc Prc	aat Asn	1651
ggc Gly	ago Ser 360	Leu	ggt Gly	gcc Ala	atg Met	cat His	Val	tac Tyr	gag Glu	ago Ser	aag Lys	FILE	cgc Arg	aac Asr	tgg Trp	1699
tcc Ser 375	Glu	ggt Gly	tac 7 Tyr	tcg Ser	gac Asp 380	) Phe	gac Asp	cgc Arg	gga Gly	gco Ala 385	ı ıyı	gtç Val	ato Ile	aco Thi	ttc r Phe 390	1747
ato Ile	cco Pro	aaq Lys	g ago s Sei	tgg r Trp 395	Ası	aco n Thi	gcc Ala	c cco	gad Asp 400	э гу	g gta s Val	a aaq l Lys	g caq s Glr	g gg n Gl; 40	c tgg y Trp 5	1795
ccg Pro		atgt:	gagc	g												1809
<21 <21	10> 11> 12> 13>	407 PRT	ptov	erti	cill	ium:	moba	raen	se							
Me	00> t Ar 1	7 g Il	e Ar	g Ar	g Ar 5	g Al	a Le	u Va	1 Ph 1	e Al	a Th	ır Me	t Se	r Al 1	.a Val 15	
Le	u Cy	s Th		.a Gl 20	y Ph	ie Me	t Pr	o Se	er Al 25	a Gl	y Gl	u Al	a Al	.a A] 80	la Asp	
As	n Gl		La G] 35	Ly Gl	u Gl	.u Th	ır Lj	/s Se 10	er Ty	r Al	la Gl	Lu Th	ır Ty 15	yr Ai	rg Leu	
Th		la A: 50	sp As	sp Va	al Al	La As	sn II 55	le As	sn Al	La Le	eu As	sn Gl 60	Lu S€	er A	la Pro	

Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser Asp Asp 70 Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile Arg 100 Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln Met 120 Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe Ala Ser 155 150 Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg Pro Arg 170 Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys Glu Ser 180 Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala Ser Val 200 Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu Asp 215 Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn Glu 230 225 Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser Phe 250 Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser Ser Ala 280 Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro Gly 300 295 Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg Ser Pro 315 310 305 Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp Phe Gly 330 Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly Asn 340 His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr Glu 365 360 355

Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg Gly 370 375 380

Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro Asp 385 390 395

Lys Val Lys Gln Gly Trp Pro 405

<210> 8

<211> 1079

<212> PRT

<213> Streptomyces albogriseolus

<400> 8

Asn Gly Glu Asn Ser Thr Ala Ala Gly Ser Ser Ala Ser Ala Thr Ala
1 5 10 15

Leu Lys Gly Lys His Arg Val Thr Leu Ile Thr Gly Asp Arg Val Ala 20 25 30

Leu Asp Ala Lys Gly Arg Val Val Gly Leu Glu Pro Ala Glu Gly Arg
35 40 45

Glu His Ile Pro Val Gln Ile Arg Arg Ser Asp Gly His Thr Leu Val 50 55 60

Val Pro Ala Asp Ala Ala Arg Leu Val Ala Ser Gly Lys Leu Asp Gln 65 70 75 80

Arg Leu Phe Asp Val Thr Glu Leu Asn Lys Ala Ala Thr Arg Thr Ala 85 90 95

His Arg Gly Gly Leu Lys Val Ile Val Gly Tyr Arg Gly Ala Ala Lys 100 105 110

Ala Ala Lys Ala Asp Val Arg Asp Ala Gly Thr Val Arg Arg Thr Leu 115 120 125

Thr Ser Leu Asn Ala Asp Ala Val Gln Thr Pro Gln Glu Ala Gly Ala 130 135 140

Glu Leu Trp Glu Ala Val Thr Asp Gly Asp Arg Thr Ala Ser Gly Val 145 150 155 160

Ala Arg Val Trp Leu Asp Gly Val Arg Lys Ala Ser Leu Asp Thr Ser 165 170 175

Val Gly Gln Ile Gly Thr Pro Lys Ala Trp Glu Ala Gly Tyr Asp Gly 180 185 190

Lys Gly Val Lys Ile Ala Val Leu Asp Thr Gly Val Asp Ala Thr His

Pro Asp Leu Lys Gly Gln Val Thr Ala Ser Lys Asn Phe Thr Ser Ala Pro Thr Thr Gly Asp Val Val Gly His Gly Thr His Val Ala Ser Ile 225 Ala Ala Gly Thr Gly Ala Gln Ser Lys Gly Thr Tyr Lys Gly Val Ala Pro Gly Ala Lys Ile Leu Asn Gly Lys Val Leu Asp Asp Ala Gly Phe Gly Asp Asp Ser Gly Ile Leu Ala Gly Met Glu Trp Ala Ala Ala Gln Gly Ala Asp Ile Val Asn Met Ser Leu Gly Gly Met Asp Thr Pro Glu 295 Thr Asp Pro Leu Glu Ala Ala Val Asp Lys Leu Ser Ala Glu Lys Gly Ile Leu Phe Ala Ile Ala Ala Gly Asn Glu Gly Pro Gln Ser Ile Gly Ser Pro Gly Ser Ala Asp Ser Ala Leu Thr Val Gly Ala Val Asp Asp Lys Asp Lys Leu Ala Asp Phe Ser Ser Thr Gly Pro Arg Leu Gly Asp 360 355 Gly Ala Val Lys Pro Asp Leu Thr Ala Pro Gly Val Asp Ile Thr Ala 375 Ala Ser Ala Lys Gly Asn Asp Ile Ala Lys Glu Val Gly Glu Lys Pro 395 Ala Gly Tyr Met Thr Ile Ser Gly Thr Ser Met Ala Thr Pro His Val 410 405 Ala Gly Ala Ala Ala Leu Leu Lys Gln Gln His Pro Glu Trp Lys Tyr 425 Ala Glu Leu Lys Gly Ala Leu Thr Ala Ser Thr Lys Asp Gly Lys Tyr 435 Thr Pro Phe Glu Gln Gly Ser Gly Arg Val Gln Val Asp Lys Ala Ile 455 Thr Gln Thr Val Ile Ala Glu Pro Val Ser Leu Ser Phe Gly Val Gln 475 470 465 Gln Trp Pro His Ala Asp Asp Lys Pro Val Thr Lys Lys Leu Thr Tyr 490 485 Arg Asn Leu Gly Thr Glu Asp Val Thr Leu Lys Leu Thr Ser Thr Ala

- Thr Gly Pro Lys Gly Lys Ala Ala Pro Ala Gly Phe Phe Thr Leu Gly 515 525
- Ala Ser Thr Leu Thr Val Pro Ala Asn Gly Thr Ala Ser Val Asp Val 530 535 540
- Thr Ala Asp Thr Arg Leu Gly Gly Ala Val Asp Gly Thr Tyr Ser Ala 545 550 560
- Tyr Val Val Ala Thr Gly Ala Gly Gln Ser Val Arg Thr Ala Ala Ala 565 570 575
- Val Glu Arg Glu Val Glu Ser Tyr Asn Val Thr Leu Lys Val Leu Asp 580 585
- Arg Ser Gly Lys Ala Thr Ala Asn Tyr Met Ala Tyr Leu Ser Gly Leu 595 600 605
- Thr Gly Leu Gly Lys Asp Arg Ser Tyr Ala Pro Tyr Glu Ala Asp Gly 610 615
- Ala Val Ser Val Arg Val Pro Lys Gly Gly Tyr Val Leu Asp Ala Ser 625 630 635 640
- Val Leu Val Gly Ala Asp Pro Glu Thr Trp Arg Gly Ala Asp Trp Leu 645 650 655
- Ala Gln Pro Lys Leu Asp Val Thr Arg Asn Thr Thr Val Thr Val Asp 660 665 670
- Ala Arg Lys Ala Lys Pro Val Lys Val Thr Val Pro Gly Lys Ala Ala 675 680 685
- Lys Ala Gln Phe Ala Ser Ala Asp Tyr Thr Ile Glu Thr Asn Asp Ser 690 695 700
- Ala Val Ser Tyr Gly Trp Trp Leu Glu Asn Tyr Ser Gly Phe Arg Ser 705 710 715 720
- Ala His Leu Gly Pro Gln Ile Thr Asn Gly Thr Leu Ser Gln Gln Trp 725 730 735
- Asn Thr His Phe Ser Asn Gly Ala Lys Ala Gln Tyr Thr Ala Ile Ser 740 745 750
- Gly Gly Lys Val Lys Lys Leu Ala Thr Gly Tyr Thr Arg Ala Phe Lys 755 760 765
- Ala Lys Glu Phe Ala Thr Val Gln Val Gly Met Gly Ala Ala Ala Ser 770 775 780
- Gly Lys Lys Gly Ala Val Thr Ala Phe Gly Trp Leu Pro Gly Ser Ser 785 790 795
- Gly Ala Ser Gly Phe Ser Gln Glu Gln Lys Leu Pro Ser Thr Arg Thr 805 810 815

Leu Tyr Leu Ser Thr Val Asn Gly Val Thr Trp Asp Leu Asp Phe Glu 820 825 830

Gln Leu Gly Gly Val Asp Asn Glu Gly Trp Pro Ile Tyr Asp Ala Val 835 840 845

Tyr Thr Ile Gly Val Gly Lys Thr Tyr Lys Gly Gly Lys Thr Tyr Lys 850 860

Glu Thr Val Asn Thr Ala Val Phe Gly Pro Arg Leu Thr Ser Ser Tyr 865 870 875 880

Gly Val Phe Arg Asp Gly Asn Ser Ile Tyr Gly Val Ile Pro Leu Phe 885 890 895

Ala Asp Gly Lys Gly His Ala Gly Ser Ser Glu Phe Ser Ser Ala Val

Thr Thr Leu Tyr Arg Asn Gly Lys Lys Val Gly Ser Asn Asn Asp Pro 915 920

Leu Phe Gly Glu Glu Gly Phe Thr Val Pro Ser Gly Asp Ala Ala Tyr 930 935 940

Arg Leu Thr Thr Ser Val Lys Arg Ser Ala Lys Val Ala Ala Ala Ser 945 950 955 960

Thr Arg Ile Asp Ala Ser Trp Thr Phe Arg Ser Lys Lys Thr Ser Gly 965 970 975

Glu Lys Gln Leu Pro Val Ser Ser Ala Arg Phe Ala Ala Val Thr Gly 980 985 990

Leu Asp Ser Lys Val Ala Ala Gly Lys Lys Ala Thr Phe Pro Val Val 995 1000 1005

Val Glu Gly Ala Ala Gln Gly Lys Asn Leu Lys Ser Leu Ala Val Tyr

Val Ser Tyr Asn Gly Gly Lys Thr Trp Lys Lys Thr Thr Val Thr Lys 1025 1030 1035 1040

Gly Lys Ile Thr Val Lys Asn Pro Ala Lys Gly Lys Ala Ile Ser Phe 1045 1050 1055

Arg Ala Lys Ile Thr Asp Lys Lys Gly Asn Ala Ser Leu Ile Thr Ile 1060 1065 1070

His Asn Ala Tyr Tyr Gly Lys 1075

<210> 9

<211> 1751

<212> DNA

<213> Streptoverticillium mobaraense

<220> <221> CDS <222> (229)..(1659) <400> 9 gctcctatga gcatcgacgc cgccagcagc gatcggttcg gtctgaccgt cgacgccgac 60 ggcgagcgcg tgtggctgga cgagcccggt cggcccgtgc cgctcgtgcg gccgtgaaag 120 gcccgaaaag agcccaagcc gtgtgaactg cgaggacaaa gggtctggcg caacgcatgt 180 caccccagat aagttcgccg cgacctttgc gaacccaggg gagggcgc atg cgc aag Met Arg Lys gct ctc aga tcg ctg ctg gcg gcg tcg atg ctc ata gga gcg atc ggc 285 Ala Leu Arg Ser Leu Leu Ala Ala Ser Met Leu Ile Gly Ala Ile Gly 5 gee gge age gee acg geg gag geg teg ate ace gee eeg cag gee 333 Ala Gly Ser Ala Thr Ala Glu Ala Ala Ser Ile Thr Ala Pro Gln Ala 25 20 gac atc aag gac cgc atc ctg aag att ccc ggg atg aag ttc gtc gag 381 Asp Ile Lys Asp Arg Ile Leu Lys Ile Pro Gly Met Lys Phe Val Glu 40 429 gag aag eee tae eag gge tae ege tae ete gtg atg aeg tae egg eag Glu Lys Pro Tyr Gln Gly Tyr Arg Tyr Leu Val Met Thr Tyr Arg Gln 60 55 ccg gtg gac cac cgc aat ccc ggc aag ggg acc ttc gag cag cgc ttc 477 Pro Val Asp His Arg Asn Pro Gly Lys Gly Thr Phe Glu Gln Arg Phe 75 acc ctg ctc cac aag gac acc gac cgg ccg acc gtg ttc ttc acg tcc 525 Thr Leu Leu His Lys Asp Thr Asp Arg Pro Thr Val Phe Phe Thr Ser 90 85 gge tae aac gte tee ace aac eec age ege age gag eec aeg ege ate 573 Gly Tyr Asn Val Ser Thr Asn Pro Ser Arg Ser Glu Pro Thr Arg Ile 110 105 100 gtg gac ggc aac cag gtg tcg atg gag tac cgg ttc ttc acg ccg tcc 621 Val Asp Gly Asn Gln Val Ser Met Glu Tyr Arg Phe Phe Thr Pro Ser 125 120 669 cgg ccg cag ccc gcc gac tgg tcc aag ctg gac atc tgg cag gcg Arg Pro Gln Pro Ala Asp Trp Ser Lys Leu Asp Ile Trp Gln Ala Ala 145 140 135 agt gac cag cac cgc ctg tac cag gcg ctg aag ccg gtc tac ggg aag 717 Ser Asp Gln His Arg Leu Tyr Gln Ala Leu Lys Pro Val Tyr Gly Lys 155 150 aac tgg ctg gcc acg ggc ggc agc aag ggc ggc atg acg gcc acc tac Asn Trp Leu Ala Thr Gly Gly Ser Lys Gly Gly Met Thr Ala Thr Tyr

165	170	175

ttc Phe 180	cgc Arg	cgc Arg	ttc Phe	Tyr	ccg Pro 185	aac Asn	gac Asp	atg Met	aac Asn	ggc Gly 190	acg Thr	gtc Val	gcc Ala	tac Tyr	gtc Val 195	813
gcg Ala	ccc Pro	aac Asn	gac Asp	gtg Val 200	aac Asn	gac Asp	aag Lys	gaa Glu	gac Asp 205	tcg Ser	gcg Ala	tac Tyr	gac Asp	aag Lys 210	ttc Phe	861
ttc Phe	cag Gln	aac Asn	gtc Val 215	ggc Gly	gac Asp	aag Lys	gcg Ala	tgc Cys 220	cgc Arg	acg Thr	cag Gln	ctc Leu	aac Asn 225	tcg Ser	gtg Val	909
cag Gln	cgc Arg	gag Glu 230	gcg Ala	ctc Leu	gtc Val	cgc Arg	cgc Arg 235	gac Asp	gag Glu	atc Ile	gtc Val	gcc Ala 240	cgc Arg	tac Tyr	gag Glu	957
aag Lys	tgg Trp 245	gct Ala	aag Lys	gag Glu	aac Asn	ggc Gly 250	aag Lys	acg Thr	ttc Phe	aag Lys	gto Val 255	. vaı	ggc Gly	agc Ser	gcc Ala	1005
gac Asp 260	Lys	gcg Ala	tac Tyr	gag Glu	aac Asn 265	gtc Val	gtc Val	ctc Leu	gac Asp	ctg Leu 270	val	tgg Trp	tcc Ser	ttc Phe	tgg Trp 275	1053
cag Gln	tac Tyr	cac His	ctg Leu	cag Gln 280	agc Ser	gac Asp	tgc Cys	gcc Ala	tcc Ser 285	Val	cco Pro	c gcc o Ala	acc Thr	aag Lys 290	ALA	1101
tcc Ser	acc Thr	gac	gag Glu 295	. Leu	tac Tyr	aag Lys	ttc Phe	atc Ile 300	Asp	gac Asp	ato	c tog e Sei	g ggc c Gly 305	PILE	gac Asp	1149
ggc	tac Tyr	acc Thi	: Asp	cag Gln	ggc Gly	ctg Leu	gag Glu 315	ιArg	tto Phe	acc Thr	c cc r Pr	g tag o Ty: 32	c tac r Tyr O	tac Ty	c cag r Glr	1197 1
gcq Ala	g ggc a Gly 325	Th:	c caq r Glr	g ctc n Leu	ggc Gly	gco Ala 330	Pro	aco Thr	gto Va	g aaq L Lys	g aa s As 33	n Pr	g cad	c cto s Le	c aaq u Lys	1245
gg( Gl <sub>2</sub> 34)	y Val	g cte	g cgg u Arg	g tad g Tyr	2 ccc 2 Pro 345	o Gl	ato / Ile	c aad e Asi	c cad	g cco n Pro 35	o Ar	c tc g Se	g ta r Ty	c gt r Va	c ccc 1 Pro 35	,
cg Ar	c gao g As	c at p Il	c cc e Pr	g ato o Med 360	t Thi	c tto	c cgo	c cco	c gg c Gl 36	y Al	g at a Me	g gc et Al	g ga .a As	c gt p Va 37	I AS	c 1341 p
cg Ar	c tg g Tr	g gt p Va	g cg l Ar 37	g Gl	g ga u Asj	c ag p Se	c cg r Ar	g aa g As: 38	n Me	g ct t Le	c tt u Ph	c gt ne Va	g ta 11 Ty 38	1 91	g ca y Gl	g 1389 n
aa As	c ga n As	c cc p Pr 39	o Tr	g ag p Se	c gg r Gl	t ga y Gl	a cc u Pr 39	o Ph	c cg e Ar	c ct g Le	g go eu G	gc aa ly Ly 40	ag gg ys Gl )0	c go y Al	cc gc .a Al	c 1437 a

gcc cgg cac gac tac cgc ttc tac gcc ccg ggc ggc aac cac ggt tcc Ala Arg His Asp Tyr Arg Phe Tyr Ala Pro Gly Gly Asn His Gly Ser 405	1485
aac atc gcc cag ttg gtg gcc gac gag cgg gcc aag gcc acg gcc gagAsn Ile Ala Gln Leu Val Ala Asp Glu Arg Ala Lys Ala Thr Ala Glu420425	1533
gtc ctg aag tgg gcc ggt gtg gcg ccg cag gcc gtc cag aag gac gag Val Leu Lys Trp Ala Gly Val Ala Pro Gln Ala Val Gln Lys Asp Glu 440 445 450	1581
aag gcc gcc aag ccg ctc gcg ccg ttc gac gcc aag ctc gac cgc gtgLys Ala Ala Lys Pro Leu Ala Pro Phe Asp Ala Lys Leu Asp Arg Val455	1629
aag aac gac aag cag agc gcg ctg cgt ccg tagggaccca gtgcgtaagg Lys Asn Asp Lys Gln Ser Ala Leu Arg Pro 470 475	1679
cggcgggcgc tcccggcgag gggcgcccgc cgtcgcgttc cggaaggccc cgggtgccgc	1739
cgccggtgct tc	1751
cyccygrydd	
<210> 10 <211> 477 <212> PRT <213> Streptoverticillium mobaraense	
<213> Streptoverticilitum mosara	
<pre>&lt;400&gt; 10 Met Arg Lys Ala Leu Arg Ser Leu Leu Ala Ala Ser Met Leu Ile Gly</pre>	
<pre>&lt;400&gt; 10 Met Arg Lys Ala Leu Arg Ser Leu Leu Ala Ala Ser Met Leu Ile Gly 1</pre>	
<pre>&lt;400&gt; 10 Met Arg Lys Ala Leu Arg Ser Leu Leu Ala Ala Ser Met Leu Ile Gly 1</pre>	
<pre>&lt;400&gt; 10 Met Arg Lys Ala Leu Arg Ser Leu Leu Ala Ala Ser Met Leu Ile Gly 1</pre>	
<pre>&lt;400&gt; 10 Met Arg Lys Ala Leu Arg Ser Leu Leu Ala Ala Ser Met Leu Ile Gly 1</pre>	
Ala Ile Arg Lys Ala Leu Arg Ser Leu Leu Ala Ala Ser Met Leu Ile Gly 10Ala Ile Gly Ala Gly Ser Ala Thr Ala 25Glu Ala Ala Ser Ile Thr Ala 30Pro Gln Ala Asp Ile Lys Asp Arg Ile Leu Lys Ile Pro Gly Met Lys 45Phe Val Glu Glu Lys Pro Tyr Gln Gly Tyr Arg Tyr Leu Val Met Thr 50Tyr Arg Gln Pro Val Asp His Arg Asn Pro Gly Lys Gly Thr Phe Glu 65Gln Arg Phe Thr Leu Leu His Lys Asp Thr Asp Arg Pro Tyr Asp 90Asp Arg Phe Thr Leu Leu His Lys Asp Thr Asp Arg Pro Thr Val Phe 95	
<pre>Adouble 10 Met Arg Lys Ala Leu Arg Ser Leu Leu Ala Ala Ser Met Leu Ile Gly 1</pre>	
<pre> Ala Ile Gly Ala Gly Ser Ala Thr Ala Glu Ala Ala Ser Met Leu Ile Gly 1</pre>	

Gln 145	Ala	Ala	Ser	Asp	Gln 150	His	Arg	Leu	Tyr	Gln 155	Ala	Leu	Lys	Pro	Val 160
Tyr	Gly	Lys	Asn	Trp 165	Leu	Ala	Thr	Gly	Gly 170	Ser	Lys	Gly	Gly	Met 175	Thr
Ala	Thr	Tyr	Phe 180	Arg	Arg	Phe	Tyr	Pro 185	Asn	Asp	Met	Asn	Gly 190	Thr	Val
Ala	Tyr	Val 195	Ala	Pro	Asn	Asp	Val 200	Asn	Asp	Lys	Glu	Asp 205	Ser	Ala	Tyr
Asp	Lys 210	Phe	Phe	Gln	Asn	Val 215	Gly	Asp	Lys	Ala	Cys 220	Arg	Thr	Gln	Leu
Asn 225	Ser	Val	Gln	Arg	Glu 230	Ala	Leu	Val	Arg	Arg 235	Asp	Glu	Ile	Val	Ala 240
Arg	Tyr	Glu	Lys	Trp 245	Ala	Lys	Glu	Asn	Gly 250	Lys	Thr	Phe	Lys	Val 255	Val
Gly	Ser	Ala	Asp 260		Ala	Tyr	Glu	Asn 265	Val	Val	Leu	Asp	Leu 270	Val	Trp
Ser	Phe	Trp 275		Tyr	His	Leu	Gln 280	Ser	Asp	Cys	Ala	Ser 285	Val	Pro	Ala
Thr	Lys 290		Ser	Thr	Asp	Glu 295	Leu	Tyr	Lys	Phe	Ile 300	Asp	Asp	Ile	Ser
Gly 305		. Asp	Gly	y Tyr	Thr 310		Gln	Gly	Leu	Glu 315	Arg	Phe	Thr	Pro	Tyr 320
Туг	Туг	Glr	n Ala	Gly 325		Gln	Leu	Gly	Ala 330	Pro	Thr	Val	Lys	Asn 335	Pro
His	: Lei	ı Lys	340		Leu	ı Arç	, Tyr	Pro 345	Gly	/ Ile	. Asn	Gln	Pro 350	Arg	Ser
Туз	r Val	l Pro 359		g Asp	o Ile	e Pro	Met 360	Thr	: Phe	e Arc	g Pro	Gly 365	Ala	Met	Ala
Ası	y Vai		o Ar	g Tr	o Val	375		ı Asp	Sei	r Arq	g Asn 380	Met	. Leu	Phe	Val
Ту: 38		y Gl	n As:	n As <sub>l</sub>	9 Pro 390		o Sei	r Gly	y Gli	u Pro 399	o Phe	e Arç	g Leu	Gly	Lys 400
Gl	y Al	a Al	a Al	a Ar 40		s As	р Ту	r Ar	g Ph	е Ту: 0	r Ala	a Pro	Gly	/ Gly	Asn

His Gly Ser Asn Ile Ala Gln Leu Val Ala Asp Glu Arg Ala Lys Ala 

Thr Ala Glu Val Leu Lys Trp Ala Gly Val Ala Pro Gln Ala Val Gln

Lys Asp Glu Lys Ala Ala Lys Pro Leu Ala Pro Phe Asp Ala Lys Leu 450 455 460	
Asp Arg Val Lys Asn Asp Lys Gln Ser Ala Leu Arg Pro 465 470 475	
<210> 11 <211> 30 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 11 gactccgacg acagggtcac ccctcccgcc	30
<210> 12 <211> 30 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 12 cgctcacatc acggccagcc ctgctttacc	30
<210> 13 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer for the promoter region and signal sequence region of S.mobaraense	
<400> 13 gtgaccctgt cgtcggagtc	20
<210> 14 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer for the promoter region and signal sequence region of S.mobaraense	

<400> 14 ggcatcctgt cgagcggctc	20
<210> 15 <211> 26 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 15 aaattcctgt gaattagctg atttag	26
<210> 16 <211> 44 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 16 gagctctccg gcgtatgcgc atagaggcga aggctccttg aata	44
<210> 17 <211> 30 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 17 atgcgcatac gccggagagc tctcgtcttc	30
<210> 18 <211> 47 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 18 ggggtgaccc tgtcgtcgga gtcgttgaag ccgttgttga tgttgaa	47
<210> 19 <211> 51 <212> DNA <213> Artificial Sequence	

```
<220>
<223> Description of Artificial Sequence: PCR primer
<400> 19
cttcgtctct tcccccgcgc cattgtcagc gaatgctggg atagcaacgc c
                                                                   51
<210> 20
<211> 51
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: PCR primer
<400> 20
cttcgtctct tcccccgcgc cattgtcctg agcgaatgct gggatagcta c
                                                                    51
<210> 21
<211> 51
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: PCR primer
 cttcgtctct tcccccgcgc cattgtcgtt gaagccgttg ttgatgttga a
                                                                    51
 <210> 22
 <211> 51
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: PCR primer
 <400> 22
 cttcgtctct tcccccgcgc cattgtcagt caggtcgcgg agggtttcct c
                                                                     51
 <210> 23
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: PCR primer
 <400> 23
                                                                     30
 gacaatggcg cgggggaaga gacgaagtcc
  <210> 24
```

٠,

<211> 25		
<212> DNA		
<213> Artificial Sequence	¢e	
<220>	Lot I I a	
<223> Description of Art	ificial Sequence:PCR primer	
<400> 24	· · · · ·	25
gcccagaagc ccaaaattga ga		
<210> 25		
<211> 52		
<212> DNA		
<213> Artificial Sequenc	ce	
<220>		
<223> Description of Art	tificial Sequence:PCR primer	
<400> 25		52
cttcgtctct tcccccgcgc ca	attgtctgc cgttgccaca ggtgcggcca gc	32
<210> 26		
<211> 52		
<212> DNA	CO	
<213> Artificial Sequence	Ce	
<220>	ngp	
<223> Description of Art	tificial Sequence:PCR primer	
<400> 26		52
cgcagccagc gatttcatgc g	tttcataga ggcgaaggct ccttgaatag gt	72
<210> 27		
<211> 30		
<212> DNA <213> Artificial Sequen	ace	
(210) Artificial bodas.		
<220>	rtificial Sequence: PCR primer	
<400> 27	ract acases	30
atgaaacgca tgaaatcgct g	ggetgeggeg	
<210> 28		
<210> 26 <211> 25		
<211> 23 <212> DNA		
<213> Artificial Sequen	nce	
<220>		
<223> Description of Ar	rtificial Sequence:PCR primer	
<400> 28		
ggatccggag cttatcgact (	gcacq	25

```
<210> 29
<211> 52
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: PCR primer
<400> 29
cgcagccagc gatttcatgc gtttcataat tctgtttcct gtgtgaaatt gt
                                                                   52
<210> 30
<211> 1461
<212> DNA
<213> Streptoverticillium cinnamoneum
<220>
<221> CDS
<222> (151)..(1398)
<400> 30
cggcggcagc cctccttgcc gccggcgcag cgacgcagga cggcgcggcc aaggccctga 60
geggeagete gtegeaaace cetecatege gtegtgetet cacatgeeet egttteaega 120
ggcttcacca caagggagtt attgatttcc atg cac aaa cgt cgg aga ctt ctc
                                  Met His Lys Arg Arg Arg Leu Leu
                                    1
gcc ttc gcc act gtg ggt gcg gtc ata tgc acc gca gga ttc aca cct
                                                                    222
Ala Phe Ala Thr Val Gly Ala Val Ile Cys Thr Ala Gly Phe Thr Pro
                          15
     10
                                                                    270
tcg gtc agc cag gcc gcc agc agt ggc gat ggg gaa gag aag ggg tcc
 Ser Val Ser Gln Ala Ala Ser Ser Gly Asp Gly Glu Glu Lys Gly Ser
 25
                      30
tac gcc gaa acg cac ggc ctg acg gcg gat gac gtc gag agc atc aac
                                                                    318
 Tyr Ala Glu Thr His Gly Leu Thr Ala Asp Asp Val Glu Ser Ile Asn
                                                           55
                                       50
                  45
 gca ctg aac gaa aga gct ctg act ctg ggc caa cct ggc aag cct ccg
                                                                    366
 Ala Leu Asn Glu Arg Ala Leu Thr Leu Gly Gln Pro Gly Lys Pro Pro
                                                       70
                                   65
 aag gaa tta cct ccg agc gcc agc gcg ccc tcc cgg gcc ccc tcc gat
                                                                     414
 Lys Glu Leu Pro Pro Ser Ala Ser Ala Pro Ser Arg Ala Pro Ser Asp
                               80
 gac egg gaa act eet eee gee gag eeg ete gae agg atg eet gag geg
                                                                     462
 Asp Arg Glu Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Glu Ala
                           95
 tac cgg gcc tac gga ggc agg gcc act acg gtc gtc aac aac tac ata
```

٠,

Tyr 105	Arg	Ala	Tyr	Gly	Gly 110	Arg	Ala	Thr	Thr	Val 115	Val	Asn	Asn	Tyr	Ile 120	
cgc Arg	aag Lys	tgg Trp	cag Gln	cag Gln 125	gtc Val	tac Tyr	agt Ser	cac His	cgc Arg 130	gac Asp	gga Gly	aag Lys	aaa Lys	cag Gln 135	caa Gln	558
atg Met	acc Thr	gaa Glu	gag Glu 140	cag Gln	cga Arg	gaa Glu	aag Lys	ctg Leu 145	tcc Ser	tac Tyr	ggt Gly	tgc Cys	gtt Val 150	ggc Gly	gtc Val	606
acc Thr	tgg Trp	gtc Val 155	aac Asn	tcg Ser	ggc Gly	ccc Pro	tac Tyr 160	ccg Pro	acg Thr	aac Asn	aga Arg	ttg Leu 165	gcg Ala	ttc Phe	gcg Ala	654
tcc Ser	ttc Phe 170	gac Asp	gag Glu	aac Asn	aag Lys	tac Tyr 175	aag Lys	aac Asn	gac Asp	ctg Leu	aag Lys 180	aac Asn	acc Thr	agc Ser	ccc Pro	702
cga Arg 185	ccc Pro	gat Asp	gaa Glu	acg Thr	cgg Arg 190	gcg Ala	gag Glu	ttc Phe	gag Glu	ggt Gly 195	cgc Arg	atc Ile	gcc Ala	aag Lys	ggc Gly 200	750
agt Ser	ttc Phe	gac Asp	gag Glu	ggg Gly 205	aag Lys	ggt Gly	ttc Phe	aag Lys	cgg Arg 210	gcg Ala	cgt Arg	gat Asp	gtg Val	gcg Ala 215	Ser	798
gtc Val	atg Met	aac Asn	aag Lys 220	Ala	ctg Leu	gaa Glu	aat Asn	gcc Ala 225	cac His	gac Asp	gag Glu	ggg Gly	act Thr 230	Tyr	atc Ile	846
aac Asn	aac Asn	cto Leu 235	Lys	acg Thr	gag Glu	ctc Leu	acg Thr 240	Asn	aac Asn	aat Asn	gac Asp	gct Ala 245	. Leu	ctc Leu	cgc Arg	894
gag Glu	gac Asp 250	Ser	cgc Arg	tcg Ser	aac Asn	ttc Phe 255	Tyr	tcg Ser	gcg Ala	r ctg Leu	agg Arg 260	, Asr	aca Thr	ccg Pro	tcc Ser	942
tto Phe 265	. Lys	g gaa s Glu	a ago ı Aro	g gad g Asp	ggc Gly 270	7 Gly	aac Asr	tac Tyr	gac Asp	c ccc Pro 275	Sei	c aaq c Lys	g ato s Met	g aag Lys	g gcg s Ala 280	990
gto Val	g ato	c tac e Ty:	c tog r Se:	g aaq r Lys 285	s His	tto Phe	c tgg e Trg	g ago Sei	ggg Gly 290	y Gli	g gad n Asp	c caq o Gli	g cgo	g ggo g Gl <u>y</u> 29!	c tcc y Ser 5	1038
tc: Se:	c gad r Ası	c aa o Ly	g ages s Ares	g Ly:	g tad s Ty	c ggo r Gl	c gad y Ası	c ccg Pro 30!	o GI	a gco u Ala	c tto a Pho	c cg e Ar	c cc g Pr 31	O AS	c cag p Gln	1086
gg Gl	t ace	c gg r Gl 31	y Le	g gt u Va	c ga l As	c ato	g tco t Se: 32	r Ly	g ga s As	c ag p Ar	a ag g Se	c at r Il 32	e Pr	g cg o Ar	c agt g Ser	1134
cc Pr	g gc o Al	c aa a Ly	g cc s Pr	c gg	c ga y Gl	a gg u Gl	t tg y Tr	g gt p Va	c aa 1 As	t tt n Ph	c ga e As	c ta p Ty	c gg r Gl	t tg y Tr	g ttc p Phe	1182

340 335 330 ggg gct caa aca gaa gcg gat gcc gac aaa acc aca tgg acc cac ggc 1230 Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Thr Trp Thr His Gly 355 350 345 gac cac tac cac gcg ccc aat agc gac ctg ggc ccc atg cac gta cac 1278 Asp His Tyr His Ala Pro Asn Ser Asp Leu Gly Pro Met His Val His 370 365 gag agc aag ttc cgg aag tgg tct gcc ggg tac gcg gac ttc gac cgc 1326 Glu Ser Lys Phe Arg Lys Trp Ser Ala Gly Tyr Ala Asp Phe Asp Arg 380 385 gga gcc tac gtg atc acg ttc ata ccc aag agc tgg aac acc gcc ccc 1374 Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro 400 395 gcc aag gtg gag caa ggc tgg ccg tgacaggctg gtactacgac ctctgctgat 1428 Ala Lys Val Glu Gln Gly Trp Pro 410 1461 ttctgcccgg tcagtccacg cctctcgacg cga <210> 31 <211> 416 <212> PRT <213> Streptoverticillium cinnamoneum Met His Lys Arg Arg Arg Leu Leu Ala Phe Ala Thr Val Gly Ala Val Ile Cys Thr Ala Gly Phe Thr Pro Ser Val Ser Gln Ala Ala Ser Ser 25 Gly Asp Gly Glu Glu Lys Gly Ser Tyr Ala Glu Thr His Gly Leu Thr Ala Asp Asp Val Glu Ser Ile Asn Ala Leu Asn Glu Arg Ala Leu Thr Leu Gly Gln Pro Gly Lys Pro Pro Lys Glu Leu Pro Pro Ser Ala Ser

His Arg Asp Gly Lys Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Lys 130 135 140

Ala Pro Ser Arg Ala Pro Ser Asp Asp Arg Glu Thr Pro Pro Ala Glu

Pro Leu Asp Arg Met Pro Glu Ala Tyr Arg Ala Tyr Gly Gly Arg Ala

Thr Thr Val Val Asn Asn Tyr Ile Arg Lys Trp Gln Gln Val Tyr Ser

Leu Ser Tyr Gly Cys Val Gly Val Thr Trp Val Asn Ser Gly Pro Tyr 150 Pro Thr Asn Arg Leu Ala Phe Ala Ser Phe Asp Glu Asn Lys Tyr Lys 170 Asn Asp Leu Lys Asn Thr Ser Pro Arg Pro Asp Glu Thr Arg Ala Glu 180 Phe Glu Gly Arg Ile Ala Lys Gly Ser Phe Asp Glu Gly Lys Gly Phe 200 Lys Arg Ala Arg Asp Val Ala Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Gly Thr Tyr Ile Asn Asn Leu Lys Thr Glu Leu Thr 230 Asn Asn Asn Asp Ala Leu Leu Arg Glu Asp Ser Arg Ser Asn Phe Tyr 250 Ser Ala Leu Arg Asn Thr Pro Ser Phe Lys Glu Arg Asp Gly Gly Asn 260 Tyr Asp Pro Ser Lys Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp 280 Ser Gly Gln Asp Gln Arg Gly Ser Ser Asp Lys Arg Lys Tyr Gly Asp 300 295 Pro Glu Ala Phe Arg Pro Asp Gln Gly Thr Gly Leu Val Asp Met Ser 315 310 Lys Asp Arg Ser Ile Pro Arg Ser Pro Ala Lys Pro Gly Glu Gly Trp 330 Val Asn Phe Asp Tyr Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Thr Trp Thr His Gly Asp His Tyr His Ala Pro Asn Ser Asp Leu Gly Pro Met His Val His Glu Ser Lys Phe Arg Lys Trp Ser 375 Ala Gly Tyr Ala Asp Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile 385 Pro Lys Ser Trp Asn Thr Ala Pro Ala Lys Val Glu Gln Gly Trp Pro 410 405

<210> 32

<211> 21

<212> DNA

<213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:PCR primer	
<400> 32 ggcgatgggg aagagaaggg g	21
<210> 33 <211> 32 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 33 ggcggatcct cgcgtcgaga ggcgtggact ga	32
<210> 34 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 34 tacgaattcg agctcggtac c	21
<210> 35 <211> 43 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 35 ccccttctct tccccatcgc ctgccgttgc cacaggtgcg gcc	43
<210> 36 <211> 26 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 36 aacggggaga acagcacggc cgccgg	26

```
<210> 37
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: PCR primer
<400> 37
                                                                    29
ggcgaattct ccggcgggcc gtcaccggt
<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: PCR primer for
      fused prepro-serineprotease construction
<400> 38
                                                                    30
ggcaagctta aattcctgtg aattagctga
<210> 39
<211> 44
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: PCR primer for
      fused prepro-serineprotease gene construction
cggccgtgct gttctccccg tttgccgttg ccacaggtgc ggcc
                                                                    44
<210> 40
<211> 20
<212> PRT
<213> Streptoverticillium mobaraence
Gln Ala Asp Ile Lys Asp Arg Ile Leu Lys Ile Pro Gly Met Lys Phe
                                       10
  1
Val Glu Glu Lys
 <210> 41
 <211> 11
 <212> PRT
 <213> Artificial Sequence
 <220>
```

```
<223> Description of Artificial Sequence:probe for svPEP
Lys Ile Pro Gly Met Lys Phe Val Glu Glu Lys
<210> 42
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:probe for svPEP
                                                                    33
aagatccccg ggatgaagtt cgtcgaggag aag
<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: PCR primer
<400> 43
                                                                    23
gaggeggegt egateacege ecc
<210> 44
<211> 32
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: PCR primer
<400> 44
                                                                     32
gccaagcttg aagcaccggc ggcggcaccc gg
 <210> 45
 <211> 46
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: PCR primer
 <400> 45
 ggggcggtga tcgacgccgc ctctgccgtt gccacaggtg cggcca
                                                                     46
 <210> 46
 <211> 37
```

<212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:PCR primer	
<400> 46 gctcggtacc caaattcctg tgaattagct gatttag	37
<210> 47	
<211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 47 gttgaagccg ttgttgatgt tgaa	24
<210> 48	
<211> 42 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 48 aacatcaaca acggcttcaa caattccgat tctgagtgcc ct	42
<210> 49	
<211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 49 cggccacgat gcgtccggcg	20
<210> 50 <211> 43	
<212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer	
<400> 50 agggcactca gaatcggaat ttgccgttgc cacaggtgcg gcc	43

```
<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: PCR primer
<400> 51
                                                                    21
aattccgatt ctgagtgccc t
<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: PCR primer
<400> 52
                                                                    20
gaattcgagc tcggtaccca
<210> 53
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: PCR primer
<400> 53
                                                                     40
agcgatttca tgcgtttcat agaggcgaag gctccttgaa
<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: PCR primer
<400> 54
                                                                     23
atgaaacgca tgaaatcgct ggc
<210> 55
 <211> 53
 <212> PRT
 <213> Homo sapiens
 <400> 55
 Asn Ser Asp Ser Gļu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
```

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn 25 Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys 40 Trp Trp Glu Leu Arg 50 <210> 56 <211> 20 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: PCR primer <400> 56 20 actgggaggc tatctccatt <210> 57 <211> 20 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: PCR primer <400> 57 20 atcgatctga tcacgttaca <210> 58 <211> 40 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: PCR primer 40 tgtaacgtga tcagatcgat tcactggtcg acaccgttga <210> 59 <211> 20 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: PCR primer <400> 59 20 acggaagcta ccttcgaggt

```
<210> 60
<211> 4
<212> PRT
<213> Streptoverticillium mobaraense
<400> 60
Phe Arg Ala Pro
1
```